

GAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGGGAGCCTGCTTTCTACTTAGGTCTCAAATTTTCCAGCCTTGTC 7

TTTGCCCTAAAATTTCTGCTGTTTATTTCAAATAGGGTCTACATACTGTGGAGCTC M M V L S  
ATG ATG GTT CTG AGT 15

G A L C F R M K D S A L K V L Y L H N N 2  
GGG GCA CTA TGC TTC CGA ATG AAG GAT TCA GCC TTG AAG GTA CTG TAT CTG CAC AAT AAC 21

Q L L A G G L H A E K V I K G E E I S V 4  
CAG CTG CTG GCT GGA GGA CTG CAC GCA GAG AAG GTC ATT AAA GGT GAG GAG ATC AGT GTT 27

V P N R A L D A S L S P V I L G V Q G G 6  
GTC CCA AAT CGG GCA CTG GAT GCC AGT CTG TCC CCT GTC ATC CTG GGC GTT CAA GGA GGA 33

S Q C L S C G T E K G P I L K L E P V N 8  
AGC CAG TGC CTA TCT TGT GGG ACA GAG AAA GGG CCA ATT CTG AAA CTT GAG CCA GTG AAC 39

I M E L Y L G A K E S K S F T F Y R R D 10  
ATC ATG GAG CTC TAC CTC GGG GCC AAG GAA TCA AAG AGC TTC ACC TTC TAC CGG CGG GAT 45

M G L T S S F E S A A Y P G W F L C T S 12  
ATG GGT CTT ACC TCC AGC TTC GAA TCC GCT GCC TAC CCA GGC TGG TTC CTC TGC ACC TCA 51

P E A D Q P V R L T Q I P E D P A W D A 14  
CCG GAA GCT GAC CAG CCT GTC AGG CTC ACT CAG ATC CCT GAG GAC CCC GCC TGG GAT GCT 57

P I T D F Y F Q Q C D \* 15  
CCC ATC ACA GAC TTC TAC TTT CAG CAG TGT GAC TAG 60

GGCTGCGTGGTCCCCAAAACCTCCATAAGCAGAGGCAGAGTAGGCAGTGGCGGCTCCTGATAGAGGATAGAGAGACAGAG 68

GAGCTCCACAGTAGGTGGCTTACTCCTCTCCTTCCCTACTGGACTCCCGCTTCTGACCTAAGGCACACAGACACTCTCT 76

TCTCCTGCATCCCAGTGCTGGTAAATCTTCTGGTATTTGGAGCTCAATGTGTAGATTCTTTTCTCAGATTGGATGGTACTAC 84

CTCTGGTGTGGAACCCAATAGAAACACGTCAGGACCAACAAAGAGCAACATAAAAGATTCTTGGGTGAAGAAGAGGTGG 92

GAACTGTTTCATACATAGTAAGATCTGACACAGTACCTCAGAAGTCCTGCCATTTCCTTATGTTCTGGAGAAAGTGGAGGG 100

GGGGTCACCAAGACTTTTCTCTGGCTGGCTGGGCCCTTTCCCTCAACCTTTCTGACATCTGCAGCCTCTCTCATTCTTGC 108

CTTCATTCTCTGGCCCTGAACCGAGAGGGTGATATCAGGATAGCTGACAGAAGATGACCAGGCACACTGTCCTGGTTTG 116

AAACCAGAGGGGACAATAAAAAACCTGATTCTGGTCTCTACTCACATAAAAAAGAAGCTTGTGAACATTAAGTGGGAAG 123

AGATTGCTACTAAATAACATACCTTGGAAATTCATCTTAATTAATAATACTTCTCTATATTATATATTTTAAAAAAA 132

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACATGCGGCCG 136

FIG. 1

Applicant: Yang Pan  
Title: NOVEL MOLECULES OF THE TANGO-93-RELATED  
PROTEIN FAMILY AND USES THEREOF  
Attorney: Jean M. Silveri  
Docket No.: MBIO98-048CP2CN1M  
Sheet 2 of 7

	M V L S G	5
ATCGACCCACGCGTCCGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAAG	ATG GTC CTG AGT GGG	71
A L C F R M K D S A L K V L Y L H N N Q		25
GCG CTG TGC TTC CGA ATG AAG GAC TCG GCA TTG AAG GTG CTT TAT CTG CAT AAT AAC CAG		131
L L A G G L H A G K V I K G E E I S V V		45
CTT CTA GCT GGA GGG CTG CAT GCA GGG AAG GTC ATT AAA GGT GAA GAG ATC AGC GTG GTC		191
P N R W L D A S L S P V I L G V Q G G S		65
CCC AAT CGG TGG CTG GAT GCC AGC CTG TCC CCC GTC ATC CTG GGT GTC CAG GGT GGA AGC		251
Q C L S C G V G Q E P T L T L E P V N I		85
CAG TSC CTG TCA TGT GGG GTG GGG CAG GAG CCG ACT CTA ACA CTA GAG CCA GTG AAC ATC		311
M E L Y L G A K E E K S F T F Y R R D M		105
ATG GAG CTC TAT CTT GGT GCC AAG GAA TCC AAG AGC TTC ACC TTC TAC CGG CGG GAC ATG		371
G L T S S F E S A A Y P G W F L C T V P		125
GGG CTC ACC TCC AGC TTC GAG TCG GCT GCC TAC CCG GGC TGG TTC CTG TGC ACG GTG CCT		431
E A D Q P V R L T Q L P E N G G W N A P		145
GAA GCC GAT CAG CCT GTC AGA CTC ACC CAG CTT CCC GAG AAT GGT GGC TGG AAT GCC CCC		491
I T D F Y F Q Q C D *		155
ATC ACA GAC TTC TAC TTC CAG CAG TGT GAC TAG		524
GGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATC		603
ACTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAGTGGGCACCTGACCACCTTTGTCTCTGGTTCCAGTTTGGATA		682
AATTCTGAGATTTGGAGCTCAGTCCACGGTCCTCCCCCACTGGATGGTGCTACTGCTGTGGAACCTTGTA AAAACCATG		761
TGGGGTAAACTGGGAATAACATGAAAAGATTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCCTGCTTAATG		840
GTAAGTGACAAGTGTTACCCCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACA		919
TGAAGTCCTGTCACTCACTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCTTGCCCCAGCCCC		998
ACCCCTTCCCTTTAATCCTGCCACTGTCATATGCTACCTTTTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAG		1077
GAGGTGGTGATGTCAGAAGAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAAC		1156
TCAGATAACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAAGACCTACTT		1235
ACCAAGTGGCATATATTGCAATTTATTTTAATTAAAGATACCTATTTATATATTTCTTTATAAAAAAAAAAAAAAAG		1314
GGCGGCCGC		1323

**FIG. 2**

```
ht93 1  MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWL 50
      |||
mt93 2  MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAEKVIKGEESISVVPNRAL 51
      |||

ht93 51 DASLSPVILGVQGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTF 100
      |||
mt93 52 DASLSPVILGVQGSQCLSCGTEKGPIKLEPVNIMELYLGAKESKSFTF 101
      |||

ht93 101 YRRDMGLTSSFESAAYPGWFLCTVPEADQPVRLTQLPENGAWNAPITDFY 150
      |||
mt93 102 YRRDMGLTSSFESAAYPGWFLCTSPEADQPVRLTQIPEDPAWDAPITDFY 151
      |||

ht93 151 FQQCD 155
      |||
mt93 152 FQQCD 156
```

**FIG. 3**

	1					50
mt93	-----	-----	-----	-----M	MVLSGALCFR	MKDSALKVLY
ht93	-----	-----	-----	-----	MVLSGALCFR	MKDSALKVLY
illra-human	MEICRGLRSH	LITLLL.FLF	HSETICRPSG	RKSSKMQAFR	IWDVNQKTFY	
illra-mouse	MEICWGPYSH	LISLLLILLF	HSEAACRPSG	KRPCKMQAFR	IWDTNQKTFY	
	51					100
mt93	LHNNQLLAGG	LHAEKVIKGE	EISVVPNRAL	DASLSPVILG	VQGSQCLSC	
ht93	LHNNQLLAGG	LHAGKVIKGE	EISVVPNRWL	DASLSPVILG	VQGSQCLSC	
illra-human	LRNNQLVAGY	LQGPVNLEE	KIDVVP....	.IEPHALFLG	IHGGKMCLSC	
illra-mouse	LRNNQLIAGY	LQGPNIKLEE	KIDMVP....	.IDLHSVFLG	IHGGKLCLSC	
	101					150
mt93	G.TEKGPIK	LEPVNIMELY	LGAKESKSFT	FYRRDMGLTS	SFESAAYPGW	
ht93	G.VGQEPTLT	LEPVNIMELY	LGAKESKSFT	FYRRDMGLTS	SFESAAYPGW	
illra-human	VKSGDETRLQ	LEAVNITDLS	ENRKQDKRFA	FIRSDSGPTT	SFESAACPGW	
illra-mouse	AKSGDDIKLQ	LEEVNITDLS	KNKEEDKRFT	FIRSEKGPTT	SFESAACPGW	
	151					186
mt93	FLCTSPEADQ	PVRLTQIPED	PAWDAPITDF	YFQQCD		
ht93	FLCTVPEADQ	PVRLTQLPEN	GGWNAPITDF	YFQQCD		
illra-human	FLCTAMEADQ	PVSLTNMPDE	G...VMVTKF	YFQEDE		
illra-mouse	FLCTTLEADR	PVSLTNTPEE	P...LIVTKF	YFQEDQ		

FIG. 4

CCACAGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAAG	M V L S	4
ATG GTC CTG AGT		74
G A L C F R M K D S A L K V L Y L H N N		24
GGG GCG CTG TGC TTC CGA ATG AAG GAC TCG GCA TTG AAG GTG CTT TAT CTG CAT AAT AAC		134
Q L L A G G L H A G K V I K G E E I S V		44
CAG CTT CTA GCT GGA GGG CTG CAT GCA GGG AAG GTC ATT AAA GGT GAA GAG ATC AGC GTG		194
V P N R W L D A S L S P V I L G V Q G G		64
GTC CCC AAT CGG TGG CTG GAT GCC AGC CTG TCC CCC GTC ATC CTG GGT GTC CAG GGT GGA		254
S Q C L S C G V G Q E P T L T L E P V N		84
AGC CAG TGC CTG TCA TGT GGG GTG GGG CAG GAG CCG ACT CTA ACA CTA GAG CCA GTG AAC		314
I M E L Y L G A K E S K S F T F Y R R D		104
ATC ATG GAG CTC TAT CTT GGT GCC AAG GAA TCC AAG AGC TTC ACC TTC TAC CGG CGG GAC		374
M G L T S S F E S A A Y P G W F L C T V		124
ATG GGG CTC ACC TCC AGC TTC GAG TCG GCT GCC TAC CCG GGC TGG TTC CTG TGC ACG GTG		434
P E A D Q P V R L T Q L P E N G G W N A		144
CCT GAA GCC GAT CAG CCT GTC AGA CTC ACC CAG CTT CCC GAG AAT GGT GGC TGG AAT GCC		494
P I T D F Y F Q Q C D *		156
CCC ATC ACA GAC TTC TAC TTC CAG CAG TGT GAC TAG		530
GGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATC		609
ACTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCAGTTTGGATA		688
AATTCTGAGATTTGGAGCTCAGTCCACGGTCCTCCCCACTGGATGGTGCTACTGCTGTGGAACCTTGTA AAAACCATG		767
TGGGGTAACTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGCTTAATG		846
GTAAGTGAAGTGTACCTGAGCCCGCAGGCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACA		925
TGAAGTCCTGTCACTCACCAGTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCTTGCCCCAGCCCC		1004
ACCCCTTCCCTTTAATCCTGCCACTGTCTATGCTACCTTTCCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAG		1083
GAGGTGGTGATGTGAGAAGAAATGGCTCGAGCTCAGAAGATAAAGATAAGTAGGGTATGCTGATCCTCTTTAAAAAC		1162
CCAAGATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAAGACCTACTT		1241
ACAAAGTGGCATATATTGCAATTTATTTTAATTAAGATACCTATTTATATTTCTTTATAGAAAAAGTCTGGAAG		1320
AGTTTACTTCAATTGTAGCAATGTGAGGTGGTGGCACTATAGGTGATTTTCTTTTAATTCTGTTAATTTATCTGTAT		1399
TTCTAATTTTTCTACAATGAAGATGAATTCCTGTATAAAAAATAAGAAAAGAAATTAATCTTGACGTAAGCAGAGCAG		1478
ACATCATCTCTGATTGTCTCAGCCTCCACTTCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTGCTGGTTGGT		1557
TGTAGTAGTGATCAGGAACAGATCTCAGCAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCT		1636
GGGTAAGGAACCTAAAGAACA AAAATCATCTGGTAATTTCTTCTAGAAGGATCACAGCCCTGGGATTC AAGGCATT		1715
GGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGAATTGTGTCCCCCTCAAATTCACATCCTTCTTGAATCTCAGTC		1794
TGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAGTTAGTTAAGACAAGGTATGCTGGATGAAGGTAGACCTAAA		1873
TTCAATATGACTGGTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGGAGACGCGGGGAAGACTATGTAAGATG		1952
AAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACCATCAGAAGCTTGAAGAGGC		2031
AAAGAAGAATTCTTCCCAAGAATAAATTCGGCTGTTTTAAGCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAC		2110
TAATACAGCTGCTAAAATGATCCCTGTCTCCTCGTGTTCATCTGTGTGTGTCCCCCTCCCAATGTACCAAAAGTTG		2189

FIG. 5A

TCTTTGTGACCAATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTCT 2268  
ACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCCATG 2347  
CTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCTGCCACAGCCACATTAGTGAACCTAGAAG 2426  
CAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTTGGTCTAACTTGTT 2490

**FIG. 5B**

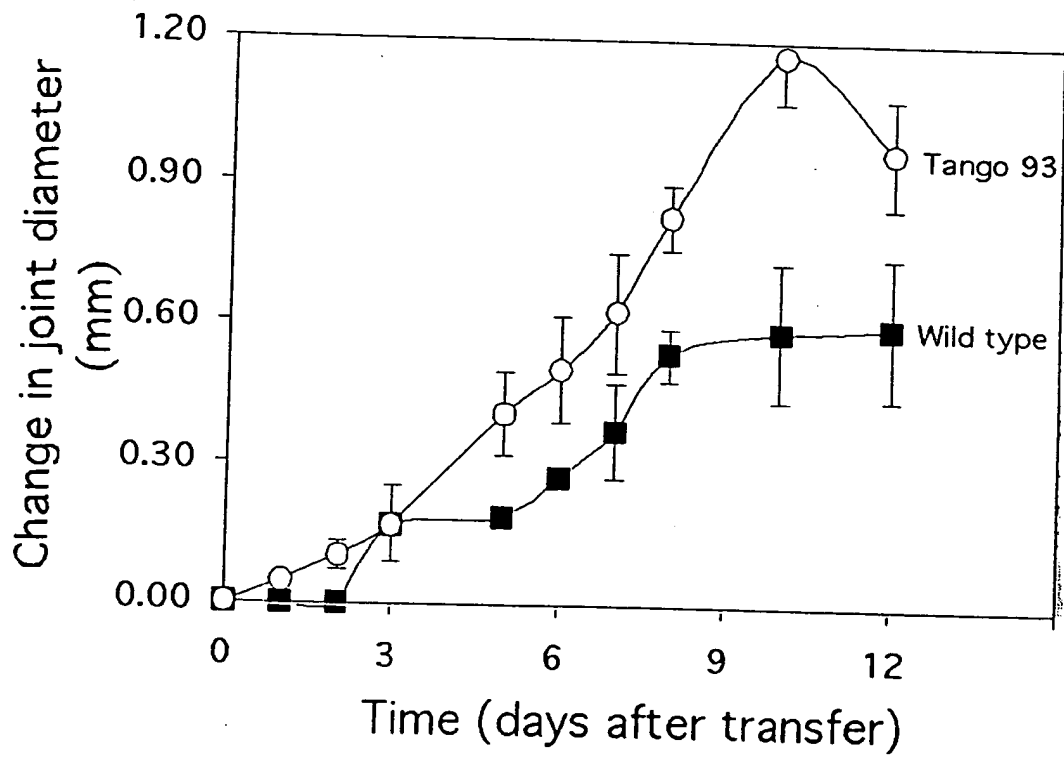


FIGURE 6